



#9

SUBSTITUTE SEQUENCE LISTING

<110> Xia, Yu-Ping et al.

<120> METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

<130> REG 710b

<140> 09/773,877

<141> 2001-01-31

<160> 27

<170> PatentIn version 3.0

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 1

gactagcagt ccggaggttag acctttcgta gagatg

36

<210> 2

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 2

cggactcaga accacatcta tgattgtatt ggt

33

<210> 3

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 3

acaatcatag atgtggttct gagtccgtct catgg

35

<210> 4

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 4

gataatgccccc gggccctttt catggaccct gacaaatg

38

<210> 5
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
gactagcagt ccggaggtag accttcgta gagatg 36

<210> 6
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
ttcctggca acagctggat atctatgatt gtattgg 38

<210> 7
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
atccagctgt tgcccaggaa gtcgctggag ctgctggta 39

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
attttcatgc acaatgacct cggtgctctc ccgaaatcg 39

<210> 9
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
tcatagatat ccagctgttg cccaggaagt cgctggag 38

<210> 10
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 10 gataatgccc gggccatttt catgcacaat gacctcggt 39

<210> 11
 <211> 1704
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Flt1(1-3)-Fc

 <220>
 <221> CDS
 <222> (1)..(1704)

<400> 11 atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc 48
 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15

tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct 96
 Cys Leu Leu Leu Thr Gly Ser Ser Gly Ser Lys Leu Lys Asp Pro
 20 25 30

gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca 144
 Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
 35 40 45

ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct 192
 Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
 50 55 60

gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc 240
 Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
 65 70 75 80

tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg aac aca 288
 Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
 85 90 95

gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta gct gta 336
 Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
 100 105 110

cct act tca aag aag gaa aca gaa tct gca atc tat ata ttt att 384
 Pro Thr Ser Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
 115 120 125

agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc ccc gaa 432
 Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
 130 135 140

att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc cg ^g gtt Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val 145 150 155 160	480
acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt gac act Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr 165 170 175	528
ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag ggc ttc Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe 180 185 190	576
atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc tgt gaa Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu 195 200 205	624
gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca cat cga Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg 210 215 220	672
caa acc aat aca atc ata gat gtc caa ata agc aca cca cgc cca gtc Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val 225 230 235 240	720
aaa tta ctt aga ggc cat act ctt gtc ctc aat tgt act gct acc act Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr 245 250 255	768
ccc ttg aac acg aga gtt caa atg acc tgg agt tac cct gat gaa aaa Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys 260 265 270	816
aat aag aga gct tcc gta agg cga cga att gac caa agc aat tcc cat Asn Lys Arg Ala Ser Val Arg Arg Ile Asp Gln Ser Asn Ser His 275 280 285	864
gcc aac ata ttc tac agt gtt ctt act att gac aaa atg cag aac aaa Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys 290 295 300	912
gac aaa gga ctt tat act tgt cgt gta agg agt gga cca tca ttc aaa Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys 305 310 315 320	960
tct gtt aac acc tca gtg cat ata tat gat aaa gca ggc ccg ggc gag Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu 325 330 335	1008
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro 340 345 350	1056
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys 355 360 365	1104
gac acc ctc atg atc tcc cg ^g acc cct gag gtc aca tgc gtg gtg gtg Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val 370 375 380	1152

gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	1200
Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	
385				390					395					400		
ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cg	gag	gag	cag	tac	1248
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	
				405					410					415		
aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	1296
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	
				420					425					430		
tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	1344
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	
				435					440					445		
cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	1392
Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	
				450					455					460		
gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cg	gat	gag	ctg	acc	aag	1440
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	
				465					470					475		480
aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	1488
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	
				485					490					495		
atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	1536
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	
				500					505					510		
acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	1584
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	
				515					520					525		
aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	1632
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	
				530					535					540		
tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	1680
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	
				545					550					555		560
ctc	tcc	ctg	tct	ccg	ggt	aaa	tga									1704
Leu	Ser	Leu	Ser	Pro	Gly	Lys										
				565												

<210> 12
 <211> 567
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Flt(1-3)-Fc

<400> 12

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
20 25 30

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
50 55 60

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65 70 75 80

Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
85 90 95

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
100 105 110

Pro Thr Ser Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
115 120 125

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
130 135 140

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
145 150 155 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
165 170 175

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
180 185 190

Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
195 200 205

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
210 215 220

Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
225 230 235 240

Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
245 250 255

Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys
260 265 270

Asn Lys Arg Ala Ser Val Arg Arg Ile Asp Gln Ser Asn Ser His
275 280 285

Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
290 295 300

Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys
305 310 315 320

Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu
325 330 335

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
340 345 350

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
355 360 365

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
370 375 380

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
385 390 395 400

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
405 410 415

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
420 425 430

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
435 440 445

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
450 455 460

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
465 470 475 480

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
485 490 495

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
500 505 510

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
515 520 525

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
530 535 540

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
545 550 555 560

Leu Ser Leu Ser Pro Gly Lys
565

<210> 13

<211> 1674

<212> DNA

<213> Artificial Sequence

<220>

<223> Flt1(1-3 ~~deltab~~) (Mut 1)

<220>

<221> CDS

<222> (1)..(1674).

<400> 13

atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc 48
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct 96
Cys Leu Leu Leu Thr Gly Ser Ser Gly Ser Lys Leu Lys Asp Pro
20 25 30

gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca 144
Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
35 40 45

ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct 192
Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
50 55 60

gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc 240
Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65 70 75 80

tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg aac aca 288
Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
85 90 95

gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta gct gta 336
Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
100 105 110

cct act tca aag aag aag gaa aca gaa tct gca atc tat ata ttt att Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile 115 120 125	384
agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc ccc gaa Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu 130 135 140	432
att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc cggtt Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val 145 150 155 160	480
acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt gac act Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr 165 170 175	528
ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag ggc ttc Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe 180 185 190	576
atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc tgt gaa Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu 195 200 205	624
gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca cat cga Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg 210 215 220	672
caa acc aat aca atc ata gat gtc caa ata agc aca cca cgc cca gtc Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val 225 230 235 240	720
aaa tta ctt aga ggc cat act ctt gtc ctc aat tgt act gct acc act Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr 245 250 255	768
ccc ttg aac acg aga gtt caa atg acc tgg agt tac cct gat gaa att Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Ile 260 265 270	816
gac caa agc aat tcc cat gcc aac ata ttc tac agt gtt ctt act att Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile 275 280 285	864
gac aaa atg cag aac aaa gac aaa gga ctt tat act tgt cgt gta agg Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg 290 295 300	912
agt gga cca tca ttc aaa tct gtt aac acc tca gtg cat ata tat gat Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp 305 310 315 320	960
aaa gca ggc ccg ggc gag ccc aaa tct tgt gac aaa act cac aca tgc Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys 325 330 335	1008
cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu 340 345 350	1056
ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag	1104

Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	
355							360					365				
gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	1152
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	
370						375				380						
ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	1200
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	
385					390				395				400			
ccg	cg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	1248
Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	
					405				410				415			
acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	1296
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	
420							425						430			
gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	1344
Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	
435						440					445					
gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	1392
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	
450						455					460					
cg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	1440
Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	
465						470				475				480		
ggc	tcc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	1488
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	
						485				490				495		
ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	1536
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	
500								505					510			
tcc	tcc	tcc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	1584
Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	
515							520					525				
cag	ggg	aac	gtc	tcc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	1632
Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	
530						535					540					
cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa	tga		1674	
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
545						550					555					

<210> 14
 <211> 557
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Flt1(1-3 ~~deltaB~~) -Fc (Mut1)

<400> 14

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
20 25 30

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
50 55 60

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65 70 75 80

Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
85 90 95

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
100 105 110

Pro Thr Ser Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
115 120 125

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
130 135 140

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
145 150 155 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
165 170 175

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
180 185 190

Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
195 200 205

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
210 215 220

Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
225 230 235 240

Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
245 250 255

Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Ile
260 265 270

Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile
275 280 285

Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg
290 295 300

Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp
305 310 315 320

Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
325 330 335

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
340 345 350

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
355 360 365

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
370 375 380

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
385 390 395 400

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
405 410 415

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
420 425 430

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
435 440 445

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
450 455 460

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
465 470 475 480

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

485

490

495

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 500 505 510

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 515 520 525

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 530 535 540

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 545 550 555

<210> 15
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> Flt1(2-3 _{deltab}) -Fc (Mut2)

<220>
<221> CDS
<222> (1)...(1359)

<400> 15
atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc 48
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc gta gag 96
Cys Leu Leu Leu Thr Gly Ser Ser Gly Gly Arg Pro Phe Val Glu
20 25 30

atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga agg gag 144
Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu
35 40 45

ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act gtt act tta 192
Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu
50 55 60

aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc ata atc 240
Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile
65 70 75 80

tgg gac agt aga aag ggc ttc atc ata tca aat gca acg tac aaa gaa 288
Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu
85 90 95

ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat ttg tat aag 336
Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys
100 105 110

aca aac tat ctc aca cat cga caa acc aat aca atc ata gat gtc caa 384
Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln

115	120	125	
ata agc aca cca cgc cca gtc aaa tta ctt aga ggc cat act ctt gtc Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val 130	135	140	432
ctc aat tgt act gct acc act ccc ttg aac acg aga gtt caa atg acc Leu Asn Cys Thr Ala Thr Pro Leu Asn Thr Arg Val Gln Met Thr 145	150	155	480
tgg agt tac cct gat gaa att gac caa agc aat tcc cat gcc aac ata Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn Ile 165	170	175	528
ttc tac agt gtt ctt act att gac aaa atg cag aac aaa gac aaa gga Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly 180	185	190	576
ctt tat act tgt cgt gta agg agt gga cca tca ttc aaa tct gtt aac Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn 195	200	205	624
acc tca gtg cat ata tat gat aaa gca ggc ccg ggc gag ccc aaa tct Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser 210	215	220	672
tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 225	230	235	720
ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 245	250	255	768
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser 260	265	270	816
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 275	280	285	864
gtg cat aat gcc aag aca aag ccg ccg gag gag gag cag tac aac agc acg Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 290	295	300	912
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 305	310	315	960
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 325	330	335	1008
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln 340	345	350	1056
gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val 355	360	365	1104

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg		1152	
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val			
370	375	380	
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct		1200	
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro			
385	390	395	400
ccc gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc		1248	
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr			
405	410	415	
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg		1296	
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val			
420	425	430	
atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg		1344	
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu			
435	440	445	
tct ccg ggt aaa tga		1359	
Ser Pro Gly Lys			
450			

<210> 16
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Flt1(2-3 deltaB)-Fc

<400> 16

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser			
1	5	10	15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu		
20	25	30

Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu		
35	40	45

Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu		
50	55	60

Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile			
65	70	75	80

Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu		
85	90	95

Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys

100 105 110
Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln
115 120 125

Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val
130 135 140

Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr
145 150 155 160

Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn Ile
165 170 175

Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly
180 185 190

Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn
195 200 205

Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 17

<211> 1389

<212> DNA

<213> Artificial Sequence

<220>

<223> Flt1(2-3)-Fc (Mut3)

<220>

<221> CDS

<222> (1)..(1389)

<400> 17

atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Ser
1 5 10 15

48

tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc gta gag
Cys Leu Leu Leu Thr Gly Ser Ser Gly Gly Arg Pro Phe Val Glu
20 25 30

96

atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga agg gag
Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu
35 40 45

144

ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act gtt act tta
Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu
50 55 60

192

aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc ata atc
Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile

240

65	70	75	80	
tgg gac agt aga aag ggc ttc atc ata tca aat gca acg tac aaa gaa Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu 85 90 95 288				
ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat ttg tat aag Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys 100 105 110 336				
aca aac tat ctc aca cat cga caa acc aat aca atc ata gat gtc caa Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln 115 120 125 384				
ata agc aca cca cgc cca gtc aaa tta ctt aga ggc cat act ctt gtc Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val 130 135 140 432				
ctc aat tgt act gct acc act ccc ttg aac acg aga gtt caa atg acc Leu Asn Cys Thr Ala Thr Pro Leu Asn Thr Arg Val Gln Met Thr 145 150 155 160 480				
tgg agt tac cct gat gaa aaa aat aag aga gct tcc gta agg cga cga Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg 165 170 175 528				
att gac caa agc aat tcc cat gcc aac ata ttc tac agt gtt ctt act Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr 180 185 190 576				
att gac aaa atg cag aac aaa gac aaa gga ctt tat act tgt cgt gta Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val 195 200 205 624				
agg agt gga cca tca ttc aaa tct gtt aac acc tca gtg cat ata tat Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr 210 215 220 672				
gat aaa gca ggc ccg ggc gag ccc aaa tct tgt gac aaa act cac aca Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr 225 230 235 240 720				
tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe 245 250 255 768				
ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cg acc cct Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro 260 265 270 816				
gag gtc aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu Val 275 280 285 864				
aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr 290 295 300 912				
aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val 305 310 315 320 960				

ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc		1008	
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys			
325	330	335	
aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc		1056	
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser			
340	345	350	
aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca		1104	
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro			
355	360	365	
tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc		1152	
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val			
370	375	380	
aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg		1200	
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly			
385	390	395	400
cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac		1248	
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp			
405	410	415	
ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg		1296	
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp			
420	425	430	
cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac		1344	
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His			
435	440	445	
aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga		1389	
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys			
450	455	460	

<210> 18
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> Flt1(2-3)-Fc (Mut3)

<400> 18

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser			
1	5	10	15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu		
20	25	30

Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu		
35	40	45

Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu

50

55

60

Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile
 65 70 75 80

Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu
 85 90 95

Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys
 100 105 110

Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln
 115 120 125

Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val
 130 135 140

Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr
 145 150 155 160

Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg
 165 170 175

Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr
 180 185 190

Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val
 195 200 205

Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr
 210 215 220

Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 225 230 235 240

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 19
<211> 1704
<212> DNA
<213> Artificial Sequence

<220>
<223> Flt1(1-3 R->N) (Mut 4)

<220>
<221> CDS
<222> (1)..(1704)

<400> 19
atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Ser
1 5 10 15

tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct
Cys Leu Leu Leu Thr Gly Ser Ser Gly Ser Lys Leu Lys Asp Pro

48

96

20	25	30	
gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr 35	40	45	144
ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro 50	55	60	192
gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala 65	70	75	240
tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg aac aca Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr 85	90	95	288
gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta gct gta Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val 100	105	110	336
cct act tca aag aag aag gaa aca gaa tct gca atc tat ata ttt att Pro Thr Ser Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile 115	120	125	384
agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc ccc gaa Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu 130	135	140	432
att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc cggtt Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val 145	150	155	480
acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt gac act Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr 165	170	175	528
ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag ggc ttc Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe 180	185	190	576
atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc tgt gaa Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu 195	200	205	624
gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca cat cga Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg 210	215	220	672
caa acc aat aca atc ata gat gtc caa ata agc aca cca cgc cca gtc Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val 225	230	235	720
aaa tta ctt aga ggc cat act ctt gtc ctc aat tgt act gct acc act Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr 245	250	255	768
ccc ttg aac acg aga gtt caa atg acc tgg agt tac cct gat gaa aaa Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys 260	265	270	816

aat aag aac gct tcc gta agg cga cga att gac caa agc aat tcc cat		864
Asn Lys Asn Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His		
275	280	285
gcc aac ata ttc tac agt gtt ctt act att gac aaa atg cag aac aaa		912
Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys		
290	295	300
gac aaa gga ctt tat act tgt cgt gta agg agt gga cca tca ttc aaa		960
Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys		
305	310	315
320		
tct gtt aac acc tca gtg cat ata tat gat aaa gca ggc ccg ggc gag		1008
Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu		
325	330	335
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct		1056
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro		
340	345	350
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag		1104
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys		
355	360	365
gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg		1152
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val		
370	375	380
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac		1200
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp		
385	390	395
400		
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac		1248
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr		
405	410	415
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac		1296
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp		
420	425	430
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc		1344
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu		
435	440	445
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga		1392
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg		
450	455	460
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag		1440
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys		
465	470	475
480		
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac		1488
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp		
485	490	495
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag		1536
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys		
500	505	510

acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc		1584	
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser			
515	520	525	
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca		1632	
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser			
530	535	540	
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc		1680	
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser			
545	550	555	560
ctc tcc ctg tct ccg ggt aaa tga		1704	
Leu Ser Leu Ser Pro Gly Lys			
565			
<210> 20			
<211> 567			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Flt1(1-3 _{R->N}) -Fc (Mut4)			
<400> 20			
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser			
1	5	10	15
Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro			
20	25	30	
Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr			
35	40	45	
Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro			
50	55	60	
Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala			
65	70	75	80
Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr			
85	90	95	
Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val			
100	105	110	
Pro Thr Ser Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile			
115	120	125	
Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu			
130	135	140	

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
145 150 155 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
165 170 175

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
180 185 190

Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
195 200 205

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
210 215 220

Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
225 230 235 240

Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
245 250 255

Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys
260 265 270

Asn Lys Asn Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His
275 280 285

Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
290 295 300

Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys
305 310 315 320

Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu
325 330 335

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
340 345 350

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
355 360 365

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
370 375 380

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
385 390 395 400

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
405 410 415

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
420 425 430

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
435 440 445

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
450 455 460

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
465 470 475 480

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
485 490 495

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
500 505 510

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
515 520 525

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
530 535 540

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
545 550 555 560

Leu Ser Leu Ser Pro Gly Lys
565

<210> 21

<211> 1453

<212> DNA

<213> Artificial Sequence

<220>

<223> Flt1D2.Flk1D3.FC_{delta}C1(a) Receptor

<220>

<221> CDS

<222> (69)..(1442)

<400> 21
 aagcttgggc tgcagggtcga tcgactctag aggatcgatc cccgggcgag ctcgaattcg 60
 caaccacc atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg 110
 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu
 1 5 10
 ctc agc tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc 158
 Leu Ser Cys Leu Leu Leu Thr Gly Ser Ser Gly Gly Arg Pro Phe 15
 20 25 30
 gta gag atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga 206
 Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly
 35 40 45
 agg gag ctc gtc att ccc tgc cggtt acg tca cct aac atc act gtt 254
 Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val
 50 55 60
 act tta aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc 302
 Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg
 65 70 75
 ata atc tgg gac agt aga aag ggc ttc atc ata tca aat gca acg tac 350
 Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr
 80 85 90
 aaa gaa ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat ttg 398
 Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu
 95 100 105 110
 tat aag aca aac tat ctc aca cat cga caa acc aat aca atc ata gat 446
 Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp
 115 120 125
 gtg gtt ctg agt ccg tct cat gga att gaa cta tct gtt gga gaa aag 494
 Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys
 130 135 140
 ctt gtc tta aat tgt aca gca aga act gaa cta aat gtg ggg att gac 542
 Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp
 145 150 155
 ttc aac tgg gaa tac cct tct tcg aag cat cag cat aag aaa ctt gta 590
 Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val
 160 165 170
 aac cga gac cta aaa acc cag tct ggg agt gag atg aag aaa ttt ttg 638
 Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu
 175 180 185 190
 agc acc tta act ata gat ggt gta acc cgg agt gac caa gga ttg tac 686
 Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr
 195 200 205
 acc tgt gca gca tcc agt ggg ctg atg acc aag aag aac agc aca ttt 734
 Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe
 210 215 220
 gtc agg gtc cat gaa aag ggc ccg ggc gac aaa act cac aca tgc cca 782
 Val Arg Val His Glu Lys Gly Pro Gly Asp Lys Thr His Thr Cys Pro

225	230	235		
ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe			830	
240	245	250		
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val			878	
255	260	265	270	
aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe			926	
275		280	285	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro			974	
290	295		300	
cg g gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr			1022	
305	310		315	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val			1070	
320	325		330	
tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala			1118	
335	340		345	350
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cg g Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg			1166	
355		360		365
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly			1214	
370	375		380	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro			1262	
385	390		395	
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser			1310	
400	405		410	
ttc ttc ctc tat agc aag ctc acc gtg gac aag agc agg tgg cag cag Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln			1358	
415	420		425	430
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His			1406	
435		440		445
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tgagcggccg c Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys			1453	
450	455			

<210> 22
<211> 458

<212> PRT
<213> Artificial Sequence

<220>
<223> Flt1D2.Flk1D3.FC_{delta}C1(a) Receptor

<400> 22

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu
20 25 30

Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu
35 40 45

Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu
50 55 60

Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile
65 70 75 80

Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu
85 90 95

Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys
100 105 110

Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Val
115 120 125

Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val
130 135 140

Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn
145 150 155 160

Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg
165 170 175

Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr
180 185 190

Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys
195 200 205

Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg

	210	215	220	
Val His Glu Lys Gly Pro Gly Asp Lys Thr His Thr Cys Pro Pro Cys				
225	230	235	240	
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro				
245	250	255		
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys				
260	265	270		
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp				
275	280	285		
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu				
290	295	300		
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu				
305	310	315	320	
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn				
325	330	335		
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly				
340	345	350		
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu				
355	360	365		
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr				
370	375	380		
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn				
385	390	395	400	
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe				
405	410	415		
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn				
420	425	430		
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr				
435	440	445		
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys				
450	455			

<210> 23
<211> 1444
<212> DNA
<213> Artificial Sequence

<220>
<223> Flt1D2.VEGFR3D3.FC_{delta}C1(a) Receptor

<220>
<221> CDS
<222> (69)..(1436)

<400> 23
aagcttgggc tgcaggcga tcgactctag aggatcgatc cccgggcgag ctcgaattcg 60
caaccacc atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg 110
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu
1 5 10

ctc agc tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc 158
Leu Ser Cys Leu Leu Leu Thr Gly Ser Ser Gly Gly Arg Pro Phe
15 20 25 30

gta gag atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga 206
Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly
35 40 45

agg gag ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act gtt 254
Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val
50 55 60

act tta aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc 302
Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg
65 70 75

ata atc tgg gac agt aga aag ggc ttc atc ata tca aat gca acg tac 350
Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr
80 85 90

aaa gaa ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat ttg 398
Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu
95 100 105 110

tat aag aca aac tat ctc aca cat cga caa acc aat aca atc ata gat 446
Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp
115 120 125

atc cag ctg ttg ccc agg aag tcg ctg gag ctg ctg gta ggg gag aag 494
Ile Gln Leu Leu Pro Arg Lys Ser Leu Glu Leu Leu Val Gly Glu Lys
130 135 140

ctg gtc ctc aac tgc acc gtg tgg gct gag ttt aac tca ggt gtc acc 542
Leu Val Leu Asn Cys Thr Val Trp Ala Glu Phe Asn Ser Gly Val Thr
145 150 155

ttt gac tgg gac tac cca ggg aag cag gca gag cggt aag tgg gtg 590
Phe Asp Trp Asp Tyr Pro Gly Lys Gln Ala Glu Arg Gly Lys Trp Val
160 165 170

ccc gag cga cgc tcc caa cag acc cac aca gaa ctc tcc agc atc ctg		638
Pro Glu Arg Arg Ser Gln Gln Thr His Thr Glu Leu Ser Ser Ile Leu		
175 180 185 190		
acc atc cac aac gtc agc cag cac gac ctg ggc tcg tat gtg tgc aag		686
Thr Ile His Asn Val Ser Gln His Asp Leu Gly Ser Tyr Val Cys Lys		
195 200 205		
gcc aac aac ggc atc cag cga ttt cg ^g gag agc acc gag gtc att gtg		734
Ala Asn Asn Gly Ile Gln Arg Phe Arg Glu Ser Thr Glu Val Ile Val		
210 215 220		
cat gaa aat ggc ccg ggc gac aaa act cac aca tgc cca ccg tgc cca		782
His Glu Asn Gly Pro Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro		
225 230 235		
gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa		830
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys		
240 245 250		
ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg		878
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val		
255 260 265 270		
gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac		926
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr		
275 280 285		
gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag		974
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu		
290 295 300		
cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac		1022
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His		
305 310 315		
cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa		1070
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys		
320 325 330		
gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag		1118
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln		
335 340 345 350		
ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg		1166
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu		
355 360 365		
acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc		1214
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro		
370 375 380		
agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac		1262
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn		
385 390 395		
tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc		1310
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu		
400 405 410		
tat agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc		1358

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val			
415	420	425	430
ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag			1406
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln			
435	440	445	
aag agc ctc tcc ctg tct ccg ggt aaa tga gcggccgc			1444
Lys Ser Leu Ser Leu Ser Pro Gly Lys			
450	455		
<210> 24			
<211> 455			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Flt1D2.VEGFR3D3.FC _{delta} C1(a)Receptor			
<400> 24			
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser			
1	5	10	15
Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu			
20	25	30	
Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu			
35	40	45	
Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu			
50	55	60	
Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile			
65	70	75	80
Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu			
85	90	95	
Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys			
100	105	110	
Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Ile Gln			
115	120	125	
Leu Leu Pro Arg Lys Ser Leu Glu Leu Leu Val Gly Glu Lys Leu Val			
130	135	140	
Leu Asn Cys Thr Val Trp Ala Glu Phe Asn Ser Gly Val Thr Phe Asp			
145	150	155	160

Trp Asp Tyr Pro Gly Lys Gln Ala Glu Arg Gly Lys Trp Val Pro Glu
165 170 175

Arg Arg Ser Gln Gln Thr His Thr Glu Leu Ser Ser Ile Leu Thr Ile
180 185 190

His Asn Val Ser Gln His Asp Leu Gly Ser Tyr Val Cys Lys Ala Asn
195 200 205

Asn Gly Ile Gln Arg Phe Arg Glu Ser Thr Glu Val Ile Val His Glu
210 215 220

Asn Gly Pro Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
290 295 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
435 440 445

Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 25

<211> 1377

<212> DNA

<213> Artificial Sequence

<220>

<223> VEGFR1R2.FC_{delta}C1(a) Receptor

<220>

<221> CDS

<222> (1)..(1377)

<400> 25

atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

48

tgt ctg ctt ctc aca gga tct agt tcc gga agt gat acc ggt aga cct
Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Asp Thr Gly Arg Pro
20 25 30

96

ttc gta gag atg tac agt gaa atc ccc gaa att ata cac atg act gaa
Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu
35 40 45

144

gga agg gag ctc gtc att ccc tgc cggtt acg tca cct aac atc act
Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr
50 55 60

192

gtt act tta aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa
Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys
65 70 75 80

240

cgc ata atc tgg gac agt aga aag ggc ttc atc ata tca aat gca acg
Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr
85 90 95

288

tac aaa gaa ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat
Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His
100 105 110

336

ttg tat aag aca aac tat ctc aca cat cga caa acc aat aca atc ata
Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile
115 120 125

384

gat	gtg	gtt	ctg	agt	ccg	tct	cat	gga	att	gaa	cta	tct	gtt	gga	gaa	432
Asp	Val	Val	Leu	Ser	Pro	Ser	His	Gly	Ile	Glu	Leu	Ser	Val	Gly	Glu	
130															140	
aag	ctt	gtc	tta	aat	tgt	aca	gca	aga	act	gaa	cta	aat	gtg	ggg	att	480
Lys	Leu	Val	Leu	Asn	Cys	Thr	Ala	Arg	Thr	Glu	Leu	Asn	Val	Gly	Ile	
145															160	
gac	tcc	aac	tgg	gaa	tac	cct	tct	tcg	aag	cat	cag	cat	aag	aaa	ctt	528
Asp	Phe	Asn	Trp	Glu	Tyr	Pro	Ser	Ser	Lys	His	Gln	His	Lys	Lys	Leu	
															175	
165																
gta	aac	cga	gac	cta	aaa	acc	cag	tct	ggg	agt	gag	atg	aag	aaa	ttt	576
Val	Asn	Arg	Asp	Leu	Lys	Thr	Gln	Ser	Gly	Ser	Glu	Met	Lys	Lys	Phe	
															190	
180																
ttg	agc	acc	tta	act	ata	gat	ggt	gtt	acc	cg	agt	gac	caa	gga	ttt	624
Leu	Ser	Thr	Leu	Thr	Ile	Asp	Gly	Val	Thr	Arg	Ser	Asp	Gln	Gly	Leu	
															205	
195																
tac	acc	tgt	gca	gca	tcc	agt	ggg	ctg	atg	acc	aag	aag	aac	agc	aca	672
Tyr	Thr	Cys	Ala	Ala	Ser	Ser	Gly	Leu	Met	Thr	Lys	Lys	Asn	Ser	Thr	
															220	
210																
ttt	gtc	agg	gtc	cat	gaa	aag	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	720
Phe	Val	Arg	Val	His	Glu	Lys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	
															240	
225																
cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	tcc	ctc	tcc	ccc	cca	768
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
															255	
245																
aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cg	acc	cct	gag	gtc	aca	tgc	816
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	
															270	
260																
gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	tcc	aac	tgg	864
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	
															285	
275																
tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cg	gag	912
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	
															300	
290																
gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	960
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	
															320	
305																
cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	1008
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
															335	
325																
aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	1056
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	
															350	
340																
cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cg	gat	gag	1104
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	
															365	
355																
ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	tcc	tat	1152

Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	
370					375					380						
ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	1200
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	
385					390					395					400	
aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	1248
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	
									405		410				415	
ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	1296
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	
									420		425				430	
gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	1344
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	
						435		440			445					
cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa	tga						1377
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
						450		455								
<210>	26															
<211>	458															
<212>	PRT															
<213>	Artificial Sequence															
<220>																
<223>	VEGFR1R2-FC _{delta} C1(a) Receptor															
<400>	26															
Met	Val	Ser	Tyr	Trp	Asp	Thr	Gly	Val	Leu	Leu	Cys	Ala	Leu	Leu	Ser	
1				5					10					15		
Cys	Leu	Leu	Leu	Thr	Gly	Ser	Ser	Ser	Gly	Ser	Asp	Thr	Gly	Arg	Pro	
					20				25				30			
Phe	Val	Glu	Met	Tyr	Ser	Glu	Ile	Pro	Glu	Ile	Ile	His	Met	Thr	Glu	
						35		40			45					
Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val	Thr	Ser	Pro	Asn	Ile	Thr	
					50		55			60						
Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	Leu	Ile	Pro	Asp	Gly	Lys	
					65		70			75			80			
Arg	Ile	Ile	Trp	Asp	Ser	Arg	Lys	Gly	Phe	Ile	Ile	Ser	Asn	Ala	Thr	
						85		90			95					
Tyr	Lys	Glu	Ile	Gly	Leu	Leu	Thr	Cys	Glu	Ala	Thr	Val	Asn	Gly	His	
					100			105			110					

Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile
115 120 125

Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
130 135 140

Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
145 150 155 160

Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
165 170 175

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
180 185 190

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
195 200 205

Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
210 215 220

Phe Val Arg Val His Glu Lys Asp Lys Thr His Thr Cys Pro Pro Cys
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
290 295 300

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
355 360 365

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 27
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide

<400> 27

Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His
1 5 10 15

Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro
20 25 30

Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro
35 40 45

Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser
50 55 60

Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val
65 70 75 80

Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn
85 90 95

Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser
100 105 110

Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn
115 120 125

Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His
130 135 140

Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met
145 150 155 160

Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp
165 170 175

Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys
180 185 190

Asn Ser Thr Phe Val Arg Val His Glu Lys Gly Pro Gly Asp Lys Thr
195 200 205

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
210 215 220

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
225 230 235 240

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
245 250 255

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
260 265 270

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
275 280 285

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
290 295 300

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
305 310 315 320

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
325 330 335

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Thr Cys Leu
340 345 350

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
355 360 365

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
370 375 380

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
385 390 395 400

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
405 410 415

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
420 425 430